

ABSTRACT

The present invention relates generally to the field of bioinformatics and its applications to functional genomics and advanced genetic engineering. More particularly, the present invention contemplates a method for identifying effector molecules capable of modulating gene network integration and which facilitate genetic multi-tasking and the regulation of complex suites of programmed responses within, on and between eukaryotic cells. The present invention permits, therefore, the identification of a new generation of proteome and nucleome modulators useful in a range of therapeutic and trait-modifying protocols. The ability to manipulate genetic networks within a cell and within whole organisms also provides a sophisticated genetic engineering approach of introducing new traits and to influencing the genetic architecture and, hence, to enable cell and organismal programming or re-programming. The identification of effector molecules and their target or receiver sites, further enables the development of diagnostic protocols for a range of conditions or physiological or genetic states of an organism useful, for example, in modulating stem cell differentiation, quantitative traits, aging or the development of pathological conditions.